

SEQUENCE LISTING

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Gardella, Thomas J.
<110>
      Kronenberg, Henry M.
      Poats, John T.
      Jupaner, Harald
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      Thereof and Novel Tethered Ligand-Receptor Molecules
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<140> US 09/475,158
<141> 1999-12-30
<150> US 60/114 577
<151> 1998-12-31
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<213> Homo sapiens

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Ser Asn Arg Lys Leu Met Glu Ile Ile 35 .

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  Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
                                   25
  gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac
                                                                     144
  Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
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55

50

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ctg to Leu Se	cg t er E	tt he	atg Met	ctg Leu 85	cgc Arg	gcc Ala	gcg Ala	agc Ser	1 1	c t e F	tc he	gtg Val	aag Lys	gac Asp	gct Ala 95	g v	tg al	288
ctc ta Leu Ty	ac t yr S	cct Ser	ggc Gly 100	ttc Phe	acg Thr	ctg Leu	gat Asp	gag Glu 105	711	c ç .a (gag Glu	cgc Arg	ctc Leu	aca Thr 110	gaq Gl	g g ı G	aa lu	336
gag t Glu L	eu l	cac His 115	atc Ile	atc Ile	gcg Ala	cag Gln	gtg Val 120	cca Pro	co Pr	ct (ccg Pro	ccg Pro	gcc Ala 125	gct Ala	gc Al	c g a A	cc la	384
gta g Val G			gct Ala	ggc	tgc Cys	cgc Arg 135	vaı	gcg Ala	g gt Vä	tg al	acc Thr	ttc Phe 140	ttc Phe	ctc	ta Ty	c t	tc he	432
ctg g Leu A 145		acc Thr	aac Asn	tac Tyr	tac Tyr 150	Trb	ato Ile	cto Lev	g g¹ u Va	u_	gag Glu 155	ggg	ctg Leu	tac Tyi	tt Le	g d u I	cac His 160	480
agc o Ser I	ctc Leu	atc Ile	ttc Phe	ato Met	: Ala	ttt Phe	tto Phe	tc: Se:		ag lu 70	aag Lys	aag Lys	tac Tyr	cto	g to u Tr 17	19 (15	ggc Gly	528
ttc a	acc Thr	atc Ile	ttt Phe	ggo Gly		g ggt	t cta y Le	a cc u Pr 18	0 7	ct la	gtc Val	ttc Phe	gto Val	gc Al 19	t gt a Va O	g al	tgg Trp	576
gtc (Val (ggt Gly	gto Val	aga Arg		a acc a Thi	tte r Le	g gc u Al 20	a As	са n T	ct hr	ggg	tgo Cys	tgg Trp 20	_	t c	tg eu	agc Ser	624
tcc Ser	ggg Gly 210			g aa s Ly	g tg s Tr	g at p Il 21	е тт	c ca e Gl	g g n V	gtg Val	ccc	ato 110 220	_	g gc u Al	a t a S	ct er	gtt Val	672
gtg Val	ctc Leu	Ası	n Ph	e Il	c ct e Le 23	u Pn	t at e Il	c aa e As	ic a sn I	atc Ile	ato 116 235		g gt g Va	g ct 1 Le	t g eu A	cc la	act Thr 240	720
225 aag Lys					c aa r As		g gg a Gl	y A	-9 '	tgt Cys 250	1.0	c ac o Th	c ag r Ar	g ca g Gl	ag c Ln G	ag 1n	tac Tyr	768
cgg Arg	aag Lys	r ct : Le	g ct u Le 26	c aç	ıg to :g S∈	c ac	eg tt ir Le	su v	tg al 65	cto Leu	gt. Va	g cc l Pr	g ct	c to	tt g he 0	gt Sly	gtg Val	816
cac His	tac Tyr	ac Th 27	c gt	•	c at ne Me	g go	La D	tg c eu P 80	cg ro	tac Tyr	c ac	c ga r Gl	ıg gt .u Va 28	c t al S 35	ca (31 y ggg	aca Thr	864
ttg Leu	Tr	g ca o Gl		tc cal	ag at ln Me	et H			ag lu	ato Met	g ct t Le		ccaa ne As	ac t sn S	cc er	ttc Phe	cag Gln	912
gga Gly	tt Ph		t g ne Va	tt g al A	cc a			ac t yr C	gt Ys	tt. Ph	c tç e C <u>y</u>	jc aa /s A:	at g sn G	gt g ly G	ag Slu	gtç Val	g cag Gln	960

305 310 315 320	
·	800
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gtg tct cac acg agt gtg acc aat gtg ggc ccc cgt gca gga ctc agc 11 Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser 355 360 365	104
ctc ccc ctc agc ccc cgc ctg cct cct gcc act acc aat ggc cac tcc 1: Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser 370 375 380	152
cag ctg cct ggc cat gcc aag cca ggg gct cca gcc act gag act gaa 1: Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu 385 390 395	200
acc cta cca gtc act atg gcg gtt ccc aag gac gat ggd tee det and Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn 410 415	248
ggc tcc tgc tca ggc ctg gat gag gag gcc tcc ggg tcc ggg tgc Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro 420 425 430	.296
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Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe	
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val	
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu	
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Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe

135

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Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
                165
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                                185
            180
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
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                            200
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
        195
                                             220
                        215
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
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                    230
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
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Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
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His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr
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                             280
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln
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Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln
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Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe
                                     330
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 Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met
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 Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser
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 Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu
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65 Leu	Ser	Ph∈	Met	Leu	70 Arg	Ala	Ala	Ser	11∈ 90	Phe	Val	L Lys	Asp	Ala 95	a Val	•
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145 Sei	Lei	ı Ile	e Phe	Met 165	Ala	Phe	e Phe	e Ser	Glu 170	д L y:	s Ly	в Ту:	r Le	u Trj 17.	o Gly	
			180	e Gly	7 Trp			192)				10	•	l Trp	
		10	l Arg	g Ala			200)				20	J		u Ser	
	2.1	y Hi	s Lys			21.	e Ile 5	e Glr			22	U			r Val	
	l Le	u As:	n Phe	e Ile	23	ı Ph	e Il	e Asr	ı Il	e Il 23	e Ar 5	g Va	l Le	u Al	a Thr 240	
22: Ly:	s Le	u Ar	g Gl	ı Thi 245	r Ası	n Al	a Gl	y Arg	g Cy 25	s As		r Ar	g Gl	n Gl 25	n Tyr 5	
Ar	g Ly	s Le	u Let 26	ı Ar	g Se	r Th	r Le	u Val 269	L Le	u Va	l Pr	o Le	u Ph 27	e Gl O	y Val	

His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr 285 280 275 Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln 300 295 290 Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln 315 310 Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala 325 <210> 40 <211> 975

<212> DNA <213> Artificial Sequence

<223> Description of Artificial Sequence: modified PTH receptor sequence

<220> <221> CDS <222> (1)..(972)

<400> 40 atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys

cca gtg ctc agc tcc gca tat gcg ctg gag gta ttt gac cgc cta ggc 96 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly

atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg 144 Met Ile Tyr Thr Vaí Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val

gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac 192 Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn 50

tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser 70

atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag 288 Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu

gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca 336 Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro 100

cet ceg ceg gee get gee gee gta gge tae get gge tge ege gtg geg 384 Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala 115

gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg 432 Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu 140 135 130

gtg Val 145	gag Glu	GJÀ ààà	ctg Leu	tac Tyr	ttg Leu 150	cac His	agc Ser	ctc Leu	atc Ile	ttc Phe 155	atg Met	gcc Ala	ttt Phe	ttc Phe	tca Ser 160	480
gag Glu	aag Lys	aag Lys	tac Tyr	ctg Leu 165	tgg Trp	ggc Gly	ttc Phe	acc Thr	atc Ile 170	ttt Phe	ggc Gly	tgg Trp	ggt Gly	cta Leu 175	ccg Pro	528
gct Ala	gtc Val	ttc Phe	gtg Val 180	gct Ala	gtg Val	tgg Trp	gtc Val	ggt Gly 185	gtc Val	aga Arg	gca Ala	acc Thr	ttg Leu 190	gcc Ala	aac Asn	576
act Thr	gly ggg	tgc Cys 195	tgg Trp	gat Asp	ctg Leu	agc Ser	tcc Ser 200	Gly ggg	cac His	aag Lys	aag Lys	tgg Trp 205	atc Ile	atc Ile	cag Gln	624
gtg Val	ccc Pro 210	atc Ile	ctg Leu	gca Ala	tct Ser	gtt Val 215	vaı	ctc Leu	aac Asn	ttc Phe	atc Ile 220	ctt Leu	ttt Phe	atc Ile	aac Asn	672
atc Ile 225	atc Ile	cgg Arg	gtg Val	ctt Leu	gcc Ala 230	act Thr	aag Lys	ctt Leu	cgg Arg	gag Glu 235	acc Thr	aat Asn	gcg Ala	ggc Gly	cgg Arg 240	720
tgt Cys	gac Asp	acc Thr	agg Arg	cag Gln 245	cag Gln	tac Tyr	cgg Arg	aag Lys	ctg Leu 250	ьеи	agg Arg	tcc Ser	acg Thr	ttg Leu 255	gtg Val	768
ctc Leu	gtg Val	ccg Pro	ctc Leu 260	Phe	ggt	gtg Val	cac His	tac Tyr 265	THE	gtc Val	ttc Phe	atg Met	gcc Ala 270	ttg Leu	ccg Pro	816
tac Tyr	acc Thr	gag Glu 275	Val	tca Ser	: GJ?	g aca Thr	ttg Lev 280	rrp	cag Gln	atc Ile	cag Gln	atg Met 285	111	tat Tyr	gag Glu	864
atg Met	cto Leu 290	Phe	aac Asn	tco Ser	tto Phe	cag Glr 295	J. GTZ	ttt Phe	ttt Phe	gtt Val	gcc Ala 300		ata Ile	tac Tyr	tgt Cys	912
tto Phe 305	e Cys	aat Asr	ggt Gly	gag Glu	g gtq 1 Val 310	L GII	g gca	ı gaç ı Glı	g att u Ile	agg Arg 315	א אורו ל	g tca Ser	tgg Trp	g ago Ser	cgc Arg 320	960
tgg Trp	g aca o Thi	cto Lev	g gcq ı Ala	g tag a	ā											975

<210> 41

<211> 324

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH receptor sequence

<400> 41

Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys 1 5 10 15 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly

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30
                                 25
             20
Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val
                                               45
                            40
Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn
                                            60
                        55
Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser
                                        75
                    70
Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu
                                    90
                85
Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro
                                105
                                                    110
           100
Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala
                                                125
                           120
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
                                            140
                        135
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
                                        155
                    150
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro
                                    170
                165
Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn
                                                    190
                                185
            180
Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln
                                                205
                            200
        195
Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn
                                            220
                        215
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
                                        235
                    230
Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val
                                    250
                245
Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro
                                265
            260
 Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu
                            280
        275
Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
                                            300
                      295
 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg
                                         315
                     310
 Trp Thr Leu Ala
 <210> 42
 <211> 9
 <212> PRT
 <213> Artificial Sequence
 <220>
 <221> UNSURE
 <222> (1)..(1)
 <223> May be any amino acid.
 <220>
 <221> UNSURE
 <222> (3)..(3)
 <223> May be any amino acid.
 <220>
 <221> UNSURE
 <222> (5)..(8)
 <223> May be any amino acid.
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<220>

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<223> Description of Artificial Sequence: synthetic
    polypeptide
<400> 42
Xaa Val Xaa Glu Xaa Xaa Xaa His
<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence
<220>
<221> UNSURE
<222> (1)..(5)
<223> May be any amino acid.
<220>
<221> UNSURE
<222> (7)..(8)
<223> May be any amino acid.
<220>
<221> UNSURE
<222> (10)
<223> May be any amino acid.
<220>
<221> UNSURE
<222> (12)
<223> May be any amino acid.
 <220>
 <221> UNSURE
 <222> (15)..(16)
 <223> May be any amino acid.
 <223> Description of Artificial Sequence: synthetic
       Polypeptide
 Xaa Xaa Xaa Xaa Arg Xaa Xaa Trp Xaa Leu Xaa Lys Leu Xaa Xaa
   1
 Val
 <210> 44
 <211> 9
 <212> PRT
 <213> Homo sapiens
 <400> 44
 Ser Val Ser Glu Ile Gln Leu Met His
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<211> 17
<212> PRT
<213> Homo sapiens
Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln
  1
Asp Val
<210> 46
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<400> 46
atgggggccg cccggatcgc acccagcctg gcgctcctac tctgctgccc agtgctcagc 60
tecgcatatg egetggtgga tgeggaegat gtetttacca aagaggaaca gatttteetg 120
<210> 47
<211> 120
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<400> 47
aaccggacgt gggccaacta cagcgagtgc ctcaagttca tgaccaatga gacccgggaa 60
cgggaggtat ttgaccgcct aggcatgatc tacaccgtgg gatactccat gtctctcgcc 120
 <210> 48
 <211> 39
 <212> RNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: modified PTH
       receptor sequence
 <400> 48
                                                                    39
 gcuguuuccg aaauccagcu gaugcacggc ggaggaggc
 <210> 49
 <211> 99
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: modified PTH
       receptor sequence
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<400> 49

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ctctgctgcc cagtgctcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac
<210> 50
<211> 99
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<400> 50
ctctgctgcc cagtgctcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac
<210> 51
<211> 96
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: synthetic
      oligonucleotide
<400> 51
ctctgctgcc cagtgctcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac
<210> 52
 <211> 96
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
 <400> 52
 ctctgctgcc cagtgctcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
 ggaggcgagg tatttgaccg cctaggcatg atctac
 <210> 53
 <211> 40
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
 <400> 53
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Val Phe
                                   25
              20
```

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Thr Lys Glu Glu Gln Ile Phe Leu
        35
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<210> 54

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH sequence

<400> 54

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr

Val Gly Tyr Ser Met Ser Leu Ala 35

<210> 55

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH sequence

<400> 55

Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln

Leu Met His Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile

Tyr

<210> 56

<211> 32

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: modified PTH sequence

<400> 56

Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp

Tyr Ala Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr 25 20

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<210> 57
<211> 1380
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: modified PTH
      receptor sequence
<220>
<221> CDS
<222> (1)..(1353)
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Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys
ece gtg etc age tec geg tac geg gtt tec gaa atc eag etg atg eat
                                                                   96
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
             20
aat cgt ggc gga ggc gag gtg ttt gac cgc ctg ggc atg att tac
                                                                   144
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
 acc gtg ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc
                                                                    192
 Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu
      50
 atc ctg gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac
                                                                    240
 Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His
  65
 atg cac ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc
                                                                    288
 Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val
 aag gac gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc
                                                                    336
 Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg
             100
 ctc acc gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct
                                                                    384
 Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro
                                                  125
         115
 gcc acc gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc
                                                                    432
 Ála Thr Ála Ála Ála Gly Tyr Ála Gly Cys Arg Val Ála Val Thr Phe
     130
 ttc ctt tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg
                                                                     480
 Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly
                                          155
                      150
  145
  ctg tac ctg cac age ctc atc ttc atg gcc ttc ttc tca gag aag aag
                                                                     528
  Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys
                                      170
  tac ctg tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc
                                                                     576
  Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe
                                  185
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gtg q Val A	Ala	gtg Val 195	tgg Trp	gtc Val	agt Ser	Val	aga Arg 200	gct Ala	acc Thr	ctg Leu	ALA .	aac Asn ' 205	acc (Thr (ggg Gly	tgc Cys	624
tgg (gac Asp 210	ttg Leu	agc Ser	tcc Ser	G] À ààà	aac Asn 215	aaa Lys	aag Lys	tgg Trp	atc Ile	atc Ile 220	cag Gln	gtg Val	ccc Pro	atc Ile	672
ctg (Leu 2 225	gcc Ala	tcc Ser	att Ile	gtg Val	ctc Leu 230	aac Asn	ttc Phe	atc Ile	ctc Leu	ttc Phe 235	atc Ile	aat Asn	atc Ile	gtc Val	cgg Arg 240	720
gtg Val	ctc Leu	gcc Ala	acc Thr	aag Lys 245	ctg Leu	cgg Arg	gag Glu	acc Thr	aac Asn 250	gcc Ala	ggc Gly	cgg Arg	tgt Cys	gac Asp 255	aca Thr	768
cgg Arg	cag Gln	cag Gln	tac Tyr 260	cgg Arg	aag Lys	ctg Leu	ctc Leu	aaa Lys 265	tcc Ser	acg Thr	ctg Leu	gtg Val	ctc Leu 270	atg Met	ccc Pro	816
ctc Leu	ttt Phe	ggc Gly 275	gtc Val	cac His	tac Tyr	att Ile	gtc Val 280	ttc Phe	atg Met	gcc Ala	aca Thr	cca Pro 285	tac Tyr	acc Thr	gag Glu	864
gtc Val	tca Ser 290	ggg	acg Thr	ctc Leu	tgg Trp	caa Gln 295	gtc Val	cag Gln	atg Met	cac His	tat Tyr 300	gag Glu	atg Met	ctc Leu	ttc Phe	912
aac Asn 305	tcc Ser	ttc Phe	cag Gln	gga Gly	ttt Phe 310	ttt Phe	gtc Val	gca Ala	atc Ile	ata Ile 315	tac Tyr	tgt Cys	ttc Phe	tgc Cys	aat Asn 320	960
ggc Gly	gag Glu	gta Val	caa Gln	gct Ala 325	GLu	atc Ile	aag Lys	aaa Lys	tct Ser 330	тгþ	agc Ser	cgc Arg	tgg Trp	aca Thr 335	ctg Leu	1008
gca Ala	ctg Leu	gac Asp	tto Phe	. Lys	cga Arg	aag Lys	gca Ala	cgc Arg 345	Ser	ggg	agc Ser	agc Ser	agc Ser 350	tat Tyr	agc Ser	1056
tac Tyr	ggc	e ccc Pro 355	Met	gtg Val	tcc Ser	cac His	aca Thr	Ser	gtg Val	acc Thr	aat Asn	gtc Val 365	ggc Gly	Pro	cgt Arg	1104
gtg Val	gga Gly 370	, Lei	ggo Gly	cto Lev	g ccc i Pro	cto Lev 375	ı Ser	ccc Pro	cgc Arg	: cta Leu	ctg Leu 380	LLO	act Thr	gco	acc Thr	1152
acc Thr 385	Asr	ggo Gly	caq Y Hi:	c cct s Pro	caç Glr 390	і Геі	g cct ı Pro	ggc Gly	cat His	gco 395	т пу-	g cca Pro	ggg	aco Thi	c cca r Pro 400	1200
gcc Ala	cto Lev	g gaq u Gl	g ac	c cto r Lev 40	u GI	g aco ı Thi	c aca	a cca r Pro	e cct Pro 410	AT	a to a Met	g gct : Ala	gct Ala	2 CC0 41	c aag c Lys 5	1248
gac Asp	gat Asp	t gg p Gl	g tt y Ph 42	e Le	c aad u Asi	c gg n Gl	c tc y Se	tgo r Cys 425	s Se	a ggo r Gl	c cto y Le	g gad ı Asp	gaç Glu 430	. 61	g gcc u Ala	1296
tct Ser	gg Gl	g cc y Pr	t ga o Gl	g cg u Ar	g cc g Pr	a cc	t gc o Al	c cto a Le	g cta u Le	a cadu Gl	g gaa n Gl	a gaç u Glu	g tgg ı Trp	g ga o Gl	g aca u Thr	1344

gtc atg tga ccaggcgctg ggggctggac ctgctga Val Met <210> 58 <211> 450 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence: modified PTH receptor sequence <400> 58 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu

Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser

Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg

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365
                            360
Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr
                                             380
                        375
Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro
                                         395
                    390
Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys
                                     410
                405
Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala
                                425
            420
Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr
                             440
        435
Val Met
    450
<210> 59
<211> 1380
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: modified PTH
       receptor sequence
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 <221> CDS
 <222> (28)..(1335)
 <400> 59
 tggatcccgc ggccctaggc ggtggcg atg ggg acc gcc cgg atc gca ccc ggc 54
                               Met Gly Thr Ala Arg Ile Ala Pro Gly
                                 1
 ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gca tat gag gtg
                                                                    102
 Leu Ala Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Glu Val
                      15
 ttt gac cgc ctg ggc atg att tac acc gtg ggc tac tcc gtg tcc ctg
                                                                    150
 Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu
 gcg tcc ctc acc gta gct gtg ctc atc ctg gcc tac ttt agg cgg ctg
 Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu
 cac tgc acg cgc aac tac atc cac atg cac ctg ttc ctg tcc ttc atg
                                                                     246
 His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met
          60
 ctg cgc gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc
                                                                     294
 Leu Arg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly
 gcc acg ctt gat gag gct gag cgc ctc acc gag gag gag ctg cgc gcc
                                                                     342
 Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala
                       95
  90
 atc gcc cag gcg ccc ccg ccg cct gcc acc gcc gcc gcc ggc tac gcg
                                                                     390
 Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala
                                      115
                  110
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ggc Gly	tgc Cys	agg Arg	gtg Val 125	gct Ala	gtg Val	acc Thr	Pne	ttc Phe 130	ctt Leu	tac Tyr	ttc Phe	ctg Leu	gcc Ala 135	acc Thr	aac Asn	438
tac Tyr	tac Tyr	tgg Trp 140	att Ile	ctg Leu	gtg Val	gag Glu	ggg Gly 145	ctg Leu	tac Tyr	ctg Leu	cac His	agc Ser 150	ctc Leu	atc Ile	ttc Phe	486
atg Met	gcc Ala 155	ttc Phe	ttc Phe	tca Ser	gag Glu	aag Lys 160	aag Lys	tac Tyr	ctg Leu	tgg Trp	ggc Gly 165	ttc Phe	aca Thr	gtc Val	ttc Phe	534
ggc Gly 170	tgg Trp	ggt Gly	ctg Leu	ccc Pro	gct Ala 175	gtc Val	ttc Phe	gtg Val	gct Ala	gtg Val 180	tgg Trp	gtc Val	agt Ser	gtc Val	aga Arg 185	582
gct Ala	acc Thr	ctg Leu	gcc Ala	aac Asn 190	acc Thr	ggg ggg	tgc Cys	tgg Trp	gac Asp 195	ttg Leu	agc Ser	tcc Ser	GJÀ ààà	aac Asn 200	aaa Lys	630
aag Lys	tgg Trp	atc Ile	atc Ile 205	cag Gln	gtg Val	ccc Pro	atc Ile	ctg Leu 210	gcc Ala	tcc Ser	att Ile	gtg Val	ctc Leu 215	aac Asn	ttc Phe	678
atc Ile	ctc Leu	ttc Phe 220	Ile	aat Asn	atc Ile	gtc Val	cgg Arg 225	gtg Val	ctc Leu	gcc Ala	acc Thr	aag Lys 230	ctg Leu	cgg Arg	gag Glu	726
acc Thr	aac Asn 235	Ala	ggc	cgg Arg	tgt Cys	gac Asp 240	aca Thr	cgg Arg	cag Gln	cag Gln	tac Tyr 245	Ary	aag Lys	ctg Leu	ctc Leu	774
aaa Lys 250	Ser	acç Thr	ctg Leu	gtg Val	ctc Leu 255	Met	ccc Pro	ctc Leu	ttt Phe	ggc Gly 260	val	cac His	tac Tyr	att Ile	gtc Val 265	822
tto Phe	ato Met	gco Ala	aca Thr	cca Pro	Туг	acc Thr	gag Glu	gtc Val	tca Ser 275	. Сту	acg Thr	cto Leu	tgg Trp	caa Glr 280	gtc Val	870
caç Gl:	g ato n Met	g cad His	tat Tyr 285	c Glu	g ato 1 Met	cto Lev	tto Phe	aac Asn 290	ı ser	ttc Phe	caç Glr	g gga	ttt Phe 295		gtc Val	918
gc: Al:	a ato a Ilo	ata = Ilo 30	e Tyı	c tgt r Cys	t tto s Phe	c tgo e Cys	aat Asr 305	1 GTZ	gaç Glu	g gta ı Val	a caa L Glr	a gct n Ala 310		g ato	aag e Lys	966
aa Ly	a tc s Se. 31	r Tr	g ago p Se:	c cgo r Aro	c tgg g Tr	g aca 7 Thi 320	с ьег	g gca ı Ala	a cto a Leo	g gad ı Asp	Phe 32	L LIY.	g cga s Arg	a aa g Ly:	g gca s Ala	1014
cg Ar 33	g Se	c gg r Gl	g ag y Se	c ag r Se	c age r Se. 33	r Ty:	t ago r Sei	c tac r Ty:	c gg r Gl	2 CC y Pro 34	J 11C	g gto	g tco l Se:	c ca r Hi	c aca s Thr 345	1062
ag Se	t gt r Va	g ac l Th	c aa r As	t gt n Va 35	I GI	c cc y Pr	c cg	t gte g Va	g gg 1 G1 35	у пе	c gg u Gl	c ct y Le	g cc	c ct o Le 36	c agc u Ser 0	1110
cc Pr	c cg	c ct g Le	a ct u Le	g cc u Pr	c ac	t gc r Al	c ac a Th	c ac r Th	c aa r As	c gg n Gl	с са у Ні	c cc s Pr	t ca o Gl	g ct n Le	g cct u Pro	1158

375 370 365 ggc cat gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca 1206 Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr 385 380 cca cct gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc 1254 Pro Pro Ála Met Ála Ála Pro Lys Ásp Ásp Gly Phe Leu Asn Gly Ser 400 395 tgc tca ggc ctg gac gag gag gcc tct ggg cct gag cgg cca cct gcc 1302 Cýs Ser Gly Leu Ásp Glu Glu Ála Ser Gly Pro Glu Arg Pro Pro Ála 420 415 ctg cta cag gaa gag tgg gag aca gtc atg tga ccaggcgctg ggggctggac 1355 Leu Leu Gln Glu Glu Trp Glu Thr Val Met 430 1380 ctgctgacat agtggatgga cagat <210> 60 <211> 435 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: modified PTH receptor sequence Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys 10 Pro Val Leu Ser Ser Ala Tyr Glu Val Phe Asp Arg Leu Gly Met Ile 30 25 20 Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val 45 40 Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile 60 5.5 His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe 75 70 Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu 90 85 Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro 110 105 100 Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr 125 120 Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu 140 135 Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys 155 150 Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val 170 165 Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly 190 185 180 Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro 205 200 Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val 195 220 215 Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp 235

230

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Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met
                                    250
                245
Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr
                                265
            260
Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu
                                                285
                            280
        275
Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys
                                            300
                        295
Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr
                                        315
                    310
Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr
                                    330
                325
Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro
                                                     350
                                345
            340
Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala
                                                 365
                            360
        355
Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr
                                             380
                        375
Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro
                                         395
                    390
Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
                                     410
                 405
Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu
                                425
 Thr Val Met
        435
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 <211> 1363
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 <223> Description of Artificial Sequence: modified PTH
       receptor sequence
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 <222> (1)..(1347)
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 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cac
                                                                    96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
              20
 ggc gga ggc gag gtg ttt gac cgc ctg ggc atg att tac acc gtg
                                                                    144
 GÍY GÍY GÍY GÍY GIÚ VaÍ Phe Ásp Arg Leu GÍY Met Ile Tyr Thr Val
 ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc atc ctg
                                                                    192
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
                           55
  gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac
                                                                     240
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
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ctg Leu	ttc Phe	ctg Leu	tcc Ser	ttc Phe 85	atg Met	ctg Leu	cgc Arg	gcc Ala	gtg Val 90	agc Ser	atc Ile	ttc Phe	gtc Val	aag Lys 95	gac Asp	288
gct Ala	gtg Val	ctc Leu	tac Tyr 100	tct Ser	ggc Gly	gcc Ala	acg Thr	ctt Leu 105	gat Asp	gag Glu	gct Ala	gag Glu	cgc Arg 110	ctc Leu	acc Thr	336
gag Glu	gag Glu	gag Glu 115	ctg Leu	cgc Arg	gcc Ala	atc Ile	gcc Ala 120	cag Gln	gcg Ala	ccc Pro	ccg Pro	ccg Pro 125	cct Pro	gcc Ala	acc Thr	384
gcc Ala	gct Ala 130	gcc Ala	ggc Gly	tac Tyr	gcg Ala	ggc Gly 135	tgc Cys	agg Arg	gtg Val	gct Ala	gtg Val 140	acc Thr	ttc Phe	ttc Phe	ctt Leu	432
tac Tyr 145	ttc Phe	ctg Leu	gcc Ala	acc Thr	aac Asn 150	tac Tyr	tac Tyr	tgg Trp	att Ile	ctg Leu 155	gtg Val	gag Glu	ggg ggg	ctg Leu	tac Tyr 160	480
ctg Leu	cac His	agc Ser	ctc Leu	atc Ile 165	ttc Phe	atg Met	gcc Ala	ttc Phe	ttc Phe 170	tca Ser	gag Glu	aag Lys	aag Lys	tac Tyr 175	ctg Leu	528
tgg Trp	ggc	ttc Phe	aca Thr 180	gtc Val	ttc Phe	ggc	tgg Trp	ggt Gly 185	ctg Leu	ccc Pro	gct Ala	gtc Val	ttc Phe 190	gtg Val	gct Ala	576
gtg Val	tgg Trp	gtc Val 195	Ser	gtc Val	aga Arg	gct Ala	acc Thr 200	Leu	gcc Ala	aac Asn	acc Thr	ggg Gly 205	tgc Cys	tgg Trp	gac Asp	624
ttg Leu	agc Ser 210	Ser	: ggg	aac Asn	aaa Lys	aag Lys 215	Trp	atc Ile	atc Ile	cag Gln	gtg Val 220	LIO	atc Ile	ctg Leu	gcc Ala	672
tcc Ser 225	Ile	gtg Val	cto Leu	: aac ı Asn	ttc Phe 230	Ile	cto	ttc Phe	atc Ile	aat Asn 235	тте	gtc Val	cgg Arg	gtg Val	ctc Leu 240	720
gcc Ala	acc Thr	aaq Lys	g ctg Lev	g cgg i Arg 245	, Glu	acc Thr	aac Asr	gco Ala	ggc Gly 250	Arg	g tgt g Cys	gac Asp	aca Thr	cgg Arg 255	OIII.	768
caç Glr	tac Tyr	cgg Arg	g aag g Lys 260	: Le	g cto Lev	aaa Lys	tco Sei	265	: Leu	gtg Val	g cto L Lev	ato Met	p ccc Pro 270	пси	ttt Phe	816
Gl ₂	gto Val	cac L Hi: 27	з Туі	c att	gto Val	tto L Phe	ato Med 280	t Ala	c aca a Thr	cca Pro	a tac o Tyr	acc Thi	c Git	gtc Val	tca Ser	864
Gl;	g acq y Thi 290	r Le	c tgg u Tr]	g caa p Gli	a gto n Val	c cag l Glr 295	n Me	g cae t Hi	c tat s Tyı	gaq Glu	g ato u Met 300	ле с	z tto u Phe	aac Asn	tcc Ser	912
tte Phe 30	e Glı	g gg n Gl	a tt y Ph	t tt e Ph	t gto e Vai	l Ala	a at	c at	a tad e Ty	c tg c Cy: 31	s Pne	c tg e Cy	c aat s Ası	ggo Gly	gag Glu 320	960
gt. Va	a caa 1 Gl:	a gc n Al	t ga a Gl	g at u Il	c aa e Ly	g aaa s Ly	a tc s Se	t tg r Tr	g age	c cg	c tg g Tr	g ac p Th	a cto	g gca ı Ala	a ctg a Leu	1008

335 330 325 1056 Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly 345 ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt gtg gga 1104 Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly 360 355 ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc acc aac 1152 Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn 375 ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca gcc ctg 1200 Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu 395 gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag gac gat 1248 Glú Thr Leu Glú Thr Thr Pro Pro Ála Met Ála Ála Pro Lys Ásp Ásp 410 405 ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc tct ggg 1296 Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly 425 cet gag egg eca eet gee etg eta eag gaa gag tgg gag aca gte atg 1344 Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met 445 440 435 1363 tga ccaggcgctg ggggct <210> 62 <211> 448 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: modified PTH receptor sequence Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Cys Cys 10 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His 25 20 Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val 40 35 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu 60 55 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His 75 70 Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp 90 Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr 105 Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Ala Thr. 100

120 Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu

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Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr
                                        155
                    150
Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu
                                    170
                165
Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala
                                185
            180
Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp
                                                205
                            200
Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala
                                            220
                        215
Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu
                                        235
                    230
Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln
                                    250
Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
                245
                                265
            260
Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
                                                 285
                            280
Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
                                             300
                        295
Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu
                                         315
                    310
Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu
                                     330
                 325
Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
                                                     350
                                 345
             340
 Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly
                                                 365
                             360
 Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn
                                             380
                         375
 Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu
     370
                                         395
                     390
 Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp
                                     410
                 405
 Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly
                                                     430
                                 425
 Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met
                             440
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<210> 63
<211> 15
<212> PRT
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<213> Homo sapiens

<210> 64 <211> 31 <212> PRT <213> Artificial Sequence

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<223> Description of Artificial Sequence: modified PTH sequence

 $<\!400\!>~64$ Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Ile Gln

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15
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                  5
  1
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
                                 25
             20
<210> 65
<211> 31
<212> PRT
<213> Artificial Sequence
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<223> Descriptilac{1}{2}n of Artificial Sequence: modified PTH
      sequence
<400> 65
Ala Val Ser Glu Has Gly Gly Gly Gly Gly Gly Gly Gly Ile Gln
Asp Leu Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
             20
 <210> 66
 <211> 31
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
 Ala Val Ser Glu His Gln Leu His Gly Gly Gly Gly Gly Gly
 <400> 66
 Asp Leu Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 <210> 67
 <211> 11
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: modified PTH
       sequence
  <400> 67
 Ala Val Ser Glu Ile Gln Leu Met His Asn Leu
                                       10
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